Amendments to the Specification

Please replace paragraph [0038] at page 8 with the following amended paragraph:

[0038] Accordingly, the present invention provides isolated TFSRPs selected from the group consisting of APS-2, ZF-2, ZF-3, ZF-4, ZF-5, MYB-1, CABF-3, SFL-1 and homologs thereof. In preferred embodiments, the TFSRP is selected from 1) a an AP2 Similar-2 (APS-2) protein as defined in SEQ ID NO:17; 2) a Zinc-Finger Factor-2 (ZF-2) protein as defined in SEQ ID NO:18; 3) a Zinc-Finger Factor-3 (ZF-3) protein as defined in SEQ ID NO:19; 4) a Zinc-Finger Factor-4 (ZF-4) protein as defined in SEQ ID NO:20; 5) a Zinc-Finger Factor-5 (ZF-5) protein as defined in SEQ ID NO:21; 6) a an MYB-1 (MYB-1) protein as defined in SEQ ID NO:22; 7) a CAAT-Box Binding Factor-3 (CABF-3) protein as defined in SEQ ID NO:23; 8) a Sigma Factor Like (SFL-1) protein as defined in SEQ ID NO:24, and homologs and orthologs thereof. Homologs and orthologs of the amino acid sequences are defined below.

Please replace paragraph [0040] at page 9 with the following amended paragraph:

[0040] The invention further provides an isolated TFSRP coding nucleic acid. The present invention includes TFSRP coding nucleic acids that encode TFSRPs as described herein. In preferred embodiments, the TFSRP coding nucleic acid is selected from 1) a an AP2 Similar-2 (APS-2) nucleic acid as defined in SEQ ID NO:9; 2) a Zinc-Finger Factor-2 (ZF-2) nucleic acid as defined in SEQ ID NO:10; 3) a Zinc-Finger Factor-3 (ZF-3) nucleic acid as defined in SEQ ID NO:11; 4) a Zinc-Finger Factor-4 (ZF-4) nucleic acid as defined in SEQ ID NO:12; 5) a Zinc-Finger Factor-5 (ZF-5) nucleic acid as defined in SEQ ID NO:13; 6) a an MYB-1 nucleic acid as defined in SEQ ID NO:14; 7) a CAAT-Box Binding Factor-3 (CABF-3) nucleic acid as defined in SEQ ID NO:15; 8) a Sigma Factor Like (SFL-1) nucleic acid as defined in SEQ ID NO:16 and homologs and orthologs thereof. Homologs and orthologs of the nucleotide sequences are defined below. In one preferred embodiment, the nucleic acid and protein are isolated from the plant genus *Physcomitrella*. In another preferred embodiment, the nucleic acid and protein are from a *Physcomitrella patens* (*P. patens*) plant.

Please replace paragraph [0056] at page 15 with the following amended paragraph:

[0056] To determine the percent homology of two amino acid sequences (e.g., one of the sequences of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 and SEQ ID NO:24 and a mutant form thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues at corresponding amino acid positions are then compared. When a position in one sequence (e.g., one of the sequences of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 and SEQ ID NO:24) is occupied by the same amino acid residue ~~as~~ at the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from the polypeptide of SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23 and SEQ ID NO:24), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The same type of comparison can be made between two nucleic acid sequences.

Please replace paragraph [0062] at page 18 with the following amended paragraph:

[0062] Finally, homology between nucleic acid sequences can also be determined using hybridization techniques known to those of skill in the art. Accordingly, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., ~~hybridizes~~ under stringent conditions, to one of the nucleotide sequences shown in SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15 and SEQ ID NO:16, or a portion thereof. More particularly, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15 or SEQ ID NO:16. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length.

Please replace paragraph [0108] at page 34 with the following amended paragraph:

[0108] For such plant transformation, binary vectors such as pBinAR can be used (Höfgen and Willmitzer, 1990 Plant Science 66:221-230). Construction of the binary vectors

can be performed by ligation of the cDNA in sense or antisense orientation into the T-DNA. 5-prime to the cDNA a plant promoter activates transcription of the cDNA. A polyadenylation sequence is located 3-prime to the cDNA. Tissue-specific expression can be achieved by using a tissue specific promoter. For example, seed-specific expression can be achieved by cloning the napin or LeB4 or USP promoter 5-prime to the cDNA. Also, any other seed specific promoter element can be used. For constitutive expression within the whole plant, the CaMV 35S promoter can be used. The expressed protein can be targeted to a cellular compartment using a signal peptide, for example for plastids, mitochondria or endoplasmic reticulum (Kermode, 1996 Crit. Rev. Plant Sci. 4 (15):285-423). The signal peptide is cloned 5-prime in frame to the cDNA to archive subcellular localization of the fusion protein. Additionally, promoters that are responsive to abiotic stresses can be used with, such as the *Arabidopsis* promoter RD29A, the nucleic acid sequences disclosed herein. One skilled in the art will recognize that the promoter used should be operatively linked to the nucleic acid such that the promoter causes transcription of the nucleic acid which results in the synthesis of a an mRNA which encodes a polypeptide. Alternatively, the RNA can be an antisense RNA for use in affecting subsequent expression of the same or another gene or genes.

Please replace paragraph [0140] at page 44 with the following amended paragraph:

[0140] Culturing was carried out in a climatic chamber at an air temperature of 25°C and light intensity of 55 ~~micromols^{-1}m^{2}~~ micromol s^{-1} m^{-2} (white light; Philips TL 65W/25 fluorescent tube) and a light/dark change of 16/8 hours. The moss was either modified in liquid culture using Knop medium according to Reski and Abel (1985, Planta 165:354-358) or cultured on Knop solid medium using 1% oxoid agar (Unipath, Basingstoke, England). The protonemas used for RNA and DNA isolation were cultured in aerated liquid cultures. The protonemas were comminuted every 9 days and transferred to fresh culture medium.

Please replace paragraph [0174] at page 64 with the following amended paragraph:

[0174] T1 seedlings were transferred to dry, sterile filter paper in a petri dish and allowed to desiccate for two hours at 80% RH (relative humidity) in a Percival Growth CU3615, ~~micromols^{-1}m^{2}~~ micromol s^{-1} m^{-2} (white light; Philips TL 65W/25 fluorescent tube). The RH was

then decreased to 60% and the seedlings were desiccated further for eight hours. Seedlings were then removed and placed on ½ MS 0.6% agar plates supplemented with 2μg/ml benomyl (Sigma-Aldrich) and 0.5g/L MES ((Sigma-Aldrich) and scored after five days.

Please replace paragraph [0175] at page 64 with the following amended paragraph:

[0175] Under drought stress conditions, PpCABF-3 over-expressing Arabidopsis thaliana plants showed ~~an~~ a 70% (39 survivors from 56 stressed plants) survival rate to the stress screening; PpZF-2, 98% (39 survivors from 40 stressed plants); PpZF-3, 94% (59 survivors from 63 stressed plants); PpZF-4, 94% (16 survivors from 17 stressed plants); PpZF-5, 80% (8 survivors from 10 stressed plants); PpAPS-2 65% (13 survivors from 20 stressed plants); and PpMYB-1 80% (8 survivors from 10 stressed plants); whereas the untransformed control a 28% (16 survivors from 57 stressed plants) survival rate. It is noteworthy that the analyses of these transgenic lines were performed with T1 plants, and therefore, the results will be better when a homozygous, strong expresser is found.

Please replace paragraphs [0196] – [0199] at pages 71-72 with the following amended paragraphs:

[0196] The constructs pBPSLVM185, pBPSSY008, pBPSSY017, pBPSLVM163, pBPSERG006, pBPSLVM161, pBPSERG001 and pBPSERG020 ~~were~~ are used to transform soybean as described below.

[0197] Seeds of soybean ~~were~~ are surface sterilized with 70% ethanol for 4 minutes at room temperature with continuous shaking, followed by 20% (v/v) Clorox supplemented with 0.05% (v/v) Tween for 20 minutes with continuous shaking. Then, the seeds ~~were~~ are rinsed 4 times with distilled water and placed on moistened sterile filter paper in a Petri dish at room temperature for 6 to 39 hours. The seed coats ~~were~~ are peeled off, and cotyledons are detached from the embryo axis. The embryo axis ~~was~~ is examined to make sure that the meristematic region is not damaged. The excised embryo axes ~~were~~ are collected in a half-open sterile Petri dish and air-dried to a moisture content less than 20% (fresh weight) in a sealed Petri dish until further use.

[0198] *Agrobacterium tumefaciens* culture ~~was~~ is prepared from a single colony in LB solid medium plus appropriate antibiotics (e.g. 100 mg/l streptomycin, 50 mg/l kanamycin) followed by growth of the single colony in liquid LB medium to an optical density at 600 nm of 0.8. Then, the ~~bacteria~~ bacterial culture ~~was~~ is pelleted at 7000 rpm for 7 minutes at room temperature, and resuspended in MS (Murashige and Skoog, 1962) medium supplemented with 100 μM acetosyringone. ~~Bacteria~~ Bacterial cultures ~~were~~ are incubated in this pre-induction medium for 2 hours at room temperature before use. The ~~axis~~ axes of soybean zygotic seed embryos at approximately 15% moisture content ~~were~~ are imbibed for 2 hours at room temperature with the pre-induced *Agrobacterium* suspension culture. The embryos are removed from the imbibition culture and ~~were~~ are transferred to Petri dishes containing solid MS medium supplemented with 2% sucrose and incubated for 2 days, in the dark at room temperature. Alternatively, the embryos ~~were~~ are placed on top of moistened (liquid MS medium) sterile filter paper in a Petri dish and incubated under the same conditions described above. After this period, the embryos ~~were~~ are transferred to either solid or liquid MS medium supplemented with 500 mg/L carbenicillin or 300mg/L cefotaxime to kill the agrobacteria. The liquid medium ~~was~~ is used to moisten the sterile filter paper. The embryos ~~were~~ are incubated ~~during~~ for 4 weeks at 25°C, under 150 μmol $m^{-2}sec^{-1}$ and 12 hours photoperiod. Once the seedlings produced roots, they ~~were~~ are transferred to sterile metromix soil. The medium of the *in vitro* plants ~~was~~ is washed off before ~~transferring~~ the plants are transferred to soil. The plants ~~were~~ are kept under a plastic cover for 1 week to favor the acclimatization process. Then the plants ~~were~~ are transferred to a growth room where they ~~were~~ are incubated at 25°C, under 150 μmol $m^{-2}sec^{-1}$ light intensity and 12 hours photoperiod for about 80 days.

[0199] The transgenic plants ~~were~~ are then screened for their improved drought, salt and/or cold tolerance according to the screening method described in Example 7 demonstrating that transgene expression confers stress tolerance.

Please replace paragraph [0200] at page 72 with the following amended paragraph:

[0200] The constructs pBPSLVM185, pBPSSY008, pBPSSY017, pBPSLVM163, pBPSERG006, pBPSLVM161, pBPSERG001 and pBPSERG020 ~~were~~ are used to transform ~~rapseed~~ rapeseed/canola as described below.

Please replace paragraph [0203] at page 73 with the following amended paragraph:

[0203] The constructs pBPSLVM185, pBPSSY008, pBPSSY017, pBPSLVM163, pBPSERG006, pBPSLVM161, pBPSERG001 and pBPSERG020 ~~were~~ are used to transform corn as described below.

Please replace paragraph [0205] at page 73 with the following amended paragraph:

[0205] The constructs pBPSLVM185, pBPSSY008, pBPSSY017, pBPSLVM163, pBPSERG006, pBPSLVM161, pBPSERG001, pBPSERG020 ~~were~~ are used to transform wheat as described below.